SEQUENCE LISTING

#7

<110> Aventis Pharma, S.A.

<120> Polyopeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754
<151> 1998-10-12

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence: Oligonucleotide

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<210> 2

<211> 29

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<213> Artificial Sequence: Oligonucleotide 3' -393 (p53)

<400> 2
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<210> 3

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ggggcagtgc ctcac 15

<210> 4

<211> 15

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<213> Artificial Sequence: Oligonucleotide W248 3'

<400> 4
gggcctccag ttcat 15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence: Oligonucleotide H273 3'

<400> 5
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<210> 6

<211> 15

<212> DNA

<213> Artificial Sequence: Oligonucleotide G281 3'

<400> 6
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<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence: Oligonucleotide 5' -73

<400> 7
agatctgtgt ggcccctgca cca 23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence: Fragment C-term MBP1 murine: CDS (1)..(885)

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cgttaccgct attgccagca tcgatgtgtg aacctgccgg gctcctttcg atgccagtgt 120

gagccaggct tccagttggg acctaacaac cgctcttgtg tggatgtgaa tgagtgtgac 180

atgggagccc catgtgagca gcgctgcttc aactcctatg ggaccttcct gtgtcgctgt 240

aaccagggct atgagctgca ccgggatggc ttctcctgca gcgatatcga tgagtgcggc 300

tactccagtt acctctgcca gtaccgctgt gtcaacgagc caggccgatt ctcctgtcac 360

tgcccacaag gctaccagct gctggctaca aggctctgcc aagatattga cgagtgtgaa 420

acaggtgcac accaatgttc tgaggcccaa acctgtgtca acttccatgg gggttaccgc 480

tgtgtggaca ccaaccgttg tgtggagccc tatgtccaag tgtcagacaa ccgctgcctc 540

tgccctgcct ccaatcccct ttgtcgagag cagccttcat ccattgtgca ccgctacatg 600

agcatcacct cagagcgaag tgtgcctgct gacgtgtttc agatccaggc aacctctgtc 660

taccctggtg cctacaatgc ctttcagatc cgttctggaa acacacaggg ggacttctac 720

attaggcaaa tcaacaatgt cagcgccatg ctggtcctcg ccaggccagt gacgggaccc 780

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aagggccatg tgggggcccc ttccccctcc catagcttaa gcagccccgg gggcctaggg 960

atgaccgttc tgcttaaagg aactatgatg tgaaggacaa taaagggaga aagaaggaaa 1020

a 1021

<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence: Fragment C-term MBP1 murine

<400> 9

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            20                  25                  30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
        35                  40                  45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
    50                  55                  60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65                  70                  75                  80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
                85                  90                  95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
            100                 105                 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
        115                 120                 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
    130                 135                 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145                 150                 155                 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
                165                 170                 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
            180                 185                 190

Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
        195                 200                 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
    210                 215                 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225                 230                 235                 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
                245                 250                 255
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Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
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Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
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Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence: Oligonucleotide c-myc 5'

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<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence: Oligonucleotide c-myc 3'

<400> 11
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<210> 12

<211> 45

<212> DNA

<213> Artificial Sequence: MCS 5'

<400> 12
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<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence: MCS 3'

<400> 13
cgcggccgca cccgggaatt gcatgcaggt cgaccga 37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence: Oligonucleotide 3' mMBP1

<400> 14
cggtactggc agaggtaact gg 22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence: MBP1 murine (complete sequence): CDS (49)..(1377)

<400> 15
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gcctcctgcc tccccgggtc tttgctgctc tgggcgtttc tgctgttgct cttgggagca 120

gcgtccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag 180

tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct 240

tgcaagggtg agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgctct 300

gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa 360

caaccaaacc cttgcccgca gggctacgag cctgatgaac aggagagctg tgtggatgtg 420

gacgagtgta cccaggcttt gcatgactgt cgccctagtc aggactgcca taaccttcct 480

ggctcctacc agtgcacctg ccctgatggt taccgaaaaa ttggacccga atgtgtggac 540

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cgatgccagt gtgagccagg cttccagttg ggacctaaca accgctcttg tgtggatgtg 660

aatgagtgtg acatgggagc cccatgtgag cagcgctgct tcaactccta tgggaccttc 720

ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatatc 780

gatgagtgcg gctactccag ttacctctgc cagtaccgct gtgtcaacga gccaggccga 840

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gacgagtgtg aaacaggtgc acaccaatgt tctgaggccc aaacctgtgt caacttccat 960

gggggttacc gctgtgtgga caccaaccgt tgtgtggagc cctatgtcca agtgtcagac 1020

aaccgctgcc tctgccctgc ctccaatccc ctttgtcgag agcagccttc atccattgtg 1080

caccgctaca tgagcatcac ctcagagcga agtgtgcctg ctgacgtgtt tcagatccag 1140

gcaacctctg tctaccctgg tgcctacaat gcctttcaga tccgttctgg aaacacacag 1200

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agctaccggg ccagctctgt actgagactc acggtctttg tgggagccta taccttctga 1380

agaccctcag ggaagggcca tgtgggggcc ccttcccccc cccatagctt aagcagcccc 1440

gggggcctag ggatgaccgt tctgcttaaa ggaactatga tgtgaaggac aataaaggga 1500

gaaagaagga aaa 1513

<210> 16

<211> 442

<212> PRT

<213> Artificial Sequence: MBP1 murine (complete sequence)

<400> 16

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Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu
            20                  25                  30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
        35                  40                  45

Ser Gln His Cys Arg Asp Tyr Asn Glu Cys Leu Thr Ile Pro Glu Ala
    50                  55                  60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65                  70                  75                  80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
                85                  90                  95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly
            100                 105                 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr
        115                 120                 125
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Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
    130                 135                 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145                 150                 155                 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
                165                 170                 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
            180                 185                 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
        195                 200                 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
    210                 215                 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225                 230                 235                 240

Cys Ser Asp Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg
                245                 250                 255

Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr
            260                 265                 270

Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr
        275                 280                 285

Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly
    290                 295                 300

Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln
305                 310                 315                 320

Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg
                325                 330                 335

Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu
            340                 345                 350

Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr
        355                 360                 365

Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly
    370                 375                 380
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Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu
385 390 395 400

Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met
405 410 415

Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg
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Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
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<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence: Oligonucleotide 3' hMBP1

<400> 17
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<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence: Oligonucleotide 5' hMBP1

<400> 18
tgtagctact ccagctacct c 21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence: Human cDNA MBP1

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aagccagccg agccgccaga gccgcgggcc gcgggggtgt cgcgggccca accccaggat 60

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cttgggatca gcttctcctc aggattctga agagcccgac agctacacgg aatgcacaga 180

tggctatgag tgggacccag acagccagca ctgccgggat gtcaacgagt gtctgaccat 240

ccctgaggcc tgcaaggggg aaatgaagtg catcaaccac tacgggggct acttgtgcct 300

gccccgctcc gctgccgtca tcaacgacct acacggcgag ggacccccgc caccagtgcc 360
tcccgctcaa caccccaacc cctgcccacc aggctatgag cccgacgatc aggacagctg 420
tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cgccccagcc aggactgcca 480
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caacttccat gggggctacc gctgcgtgga caccaaccgc tgcgtggagc cctacatcca 1020
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atccattgtg caccgctaca tgaccatcac ctcggagcgg ag 1122

<210> 20
<211> 684
<212> DNA
<213> Artificial Sequence: Human cDNA MBP1 (partial sequence)

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taccgctgcg tggacaccaa ccgctgcgtg gagccctaca tccaggtctc tgagaaccgc 240
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tacatgacca tcacctcgga gcggagcgtg cccgctgacg tgttccagat ccaggcgacc 360
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ggcccccggg agtacgtgct ggacctggag atggtcacca tgaattccct catgagctac 540
cgggccagct ctgtactgag gctcaccgtc tttgtagggg cctacacctt ctgaggagca 600
ggagggagcc accctccctg cagctaccct agctgaggag cctgttgtga ggggcagaat 660
gagaaaggca ataaagggag aaag 684

<210> 21

<211> 1422

<212> DNA

<213> Artificial Sequence: Human MBP1 (complete sequence): CDS (59)..(1387)

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gatggctatg agtgggaccc agacagccag cactgccggg atgtcaacga gtgtctgacc 180

atccctgagg cctgcaaggg ggaaatgaag tgcatcaacc actacggggg ctacttgtgc 240

ctgccccgct ccgctgccgt catcaacgac ctacacggcg agggaccccc gccaccagtg 300

cctcccgctc aacaccccaa cccctgccca ccaggctatg agcccgacga tcaggacagc 360

tgtgtggatg tggacgagtg tgcccaggcc ctgcacgact gtcgccccag ccaggactgc 420

cataacttgc ctggctccta tcagtgcacc tgccctgatg gttaccgcaa gatcgggccc 480

gagtgtgtgg acatagacga gtgccgctac cgctactgcc agcaccgctg cgtgaacctg 540

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tgttgtgagg ggcagaatga gaaaggcaat aaagggagaa ag 1422

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence: Human MBP1 (complete sequence)

<400> 22

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Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu
            20                  25                  30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
        35                  40                  45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
    50                  55                  60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65                  70                  75                  80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
                85                  90                  95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
            100                 105                 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
        115                 120                 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
    130                 135                 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145                 150                 155                 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
                165                 170                 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
            180                 185                 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
        195                 200                 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
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210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Phe Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
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<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence: cDNA MBP1 murine (partial sequence)

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gcgtccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag 180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct 240
tgcaagggtg agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgctct 300
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aatgagtgtg acatgggagc cccatgtgag cagcgctgct tcaactccta tgggaccttc 720
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gatgagtgcg gctactccag ttacctctgc cagtacc 817

<210> 24
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<212> DNA
<213> Artificial Sequence: Oligonucleotide sens-GAPDH

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<210> 25
<211> 24
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<213> Artificial Sequence: Oligonucleotide antisens-GAPDH

<400> 25
agccttctcc atggtggtga agac 24

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence: Oligonucleotide

<400> 26
cggttggcct tggggttcag ggggg 25

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence: Oligonucleotide sens MBP1

<400> 27
gccctgatgg ttaccgcaag a 21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence: Oligonucleotide antisens MBP1

<400> 28
agcccccatg gaagttgaca c 21

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence: Oligonucleotide sens actine

<400> 29
gtggggcgcc ccaggcacca 20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence: Human fragment C-term MBP1: CDS
(1)..(885)

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cgctaccgct actgccagca ccgctgcgtg aacctgcctg gctccttccg ctgccagtgc 120

gagccgggct tccagctggg gcctaacaac cgctcctgtg ttgatgtgaa cgagtgtgac 180

atgggggccc catgcgagca gcgctgcttc aactcctatg ggaccttcct gtgtcgctgc 240

caccagggct atgagctgca tcgggatggc ttctcctgca gtgatattga tgagtgtagc 300

tactccagct acctctgtca gtaccgctgc gtcaacgagc caggccgttt ctcctgccac 360

tgcccacagg gttaccagct gctggccaca cgcctctgcc aagacattga tgagtgtgag 420

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tgcgtggaca ccaaccgctg cgtggagccc tacatccagg tctctgagaa ccgctgtctc 540

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cctcaggctg gggcagggtg gcacttgggg gggcaggcca agttcaccta aatgggggtc 1080

tctatatgtt caggcccagg ggcccccatt gacaggagct gggagctctg caccacgagc 1140

ttcagtcacc ccgagaggag aggaggtaac gaggagggcg gactccaggc cccggcccag 1200

agatttggac ttggctggct tgcaggggtc ctaagaaact ccactctgga cagcgccagg 1260

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<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence: Human fragment C-term MBP1

<400> 31

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Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
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Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
        35                  40                  45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
    50                  55                  60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65                  70                  75                  80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
                85                  90                  95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
            100                 105                 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
        115                 120                 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
    130                 135                 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145                 150                 155                 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu
                165                 170                 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
            180                 185                 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val
        195                 200                 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
    210                 215                 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr
225                 230                 235                 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
                245                 250                 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
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Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
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Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence: Fragment c-term fibuline 2 murine: CDS (1)..(999)

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agggatgcat tcggcaggac ttgcattgat gtgaacgaat gctgggtctc gccgggccgc 180

ctgtgccagc acacatgtga gaacacaccg ggctcctacc gctgctcctg cgctgctggc 240

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tgcagccagg aatgtgccaa catctatggc tcctatcagt gctactgccg tcagggctac 360

cagctggcag aggatgggca tacctgcaca gacatcgatg agtgtgcaca gggcgcgggc 420

attctctgta ccttccgctg tgtcaacgtg cctgggagct accagtgtgc atgcccagag 480

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acatgccagg atatcacgga atgtcaaacc tcaccagctc gcatcacgca ctaccagctc 720

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gactctgtaa cttaacttaa tcatgctgag ctggttggtc ttgagtctct accctagagg 1140

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gttccaggcc agcctggtct acactgggag ttctaaccag ccagagctac atagagagac 1440

cctatctcaa caaggaaaaa acgaaagaaa tctctgtgag ttccaggcca gcctggtcta 1500

cgctgggagt tctaaccagc cagagctaca tagagagatc ctatctcaac aaggaaaaat 1560

gaaagaaatc attttaaaag gttttttttt ttgctgttgt tgtttaatga taagagtagc 1620

acatatacat tattaaaaat gatcaaatag cacagaaagg tta 1663

<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence: Fragment c-term fibuline 2 murine

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
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Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
65 70 75 80

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu

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145                 150                 155                 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp
                165                 170                 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His
            180                 185                 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn
        195                 200                 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp
    210                 215                 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu
225                 230                 235                 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly
                245                 250                 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys
            260                 265                 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr
        275                 280                 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
    290                 295                 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
305                 310                 315                 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro
                325                 330
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